

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number:

09/SS4,860D

Source:

FFW/6

Date Processed by STIC:

7-19-06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/19/2006

PATENT APPLICATION: US/09/554,860D

TIME: 13:21:54

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\04192006\I554860D.raw

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4 <110> APPLICANT: Smithkline Beecham Biologicals s.a.
5      Bollen, Alex
6      Bruck, Claudine
7      Jacobs, Paul
8      Massaer, Marc
10 <120> TITLE OF INVENTION: Recombinant Allergen With Reduced Enzymatic Activity
13 <130> FILE REFERENCE: B45122
15 <140> CURRENT APPLICATION NUMBER: US 09/554,860D
16 <141> CURRENT FILING DATE: 2000-05-19
18 <150> PRIOR APPLICATION NUMBER: PCT/EP98/07521
19 <151> PRIOR FILING DATE: 1998-11-16
21 <150> PRIOR APPLICATION NUMBER: GB9724531.0
22 <151> PRIOR FILING DATE: 1997-11-19
24 <160> NUMBER OF SEQ ID NOS: 31
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 320
30 <212> TYPE: PRT
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Recombinant mutant Der p1 including pre-protein -
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37 <400> SEQUENCE: 1
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39 1          5          10          15
40 Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala
41          20          25          30
42 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
43          35          40          45
44 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
45          50          55          60
46 Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
47 65          70          75          80
48 Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
49          85          90          95
50 Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile
51          100         105         110
52 Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly
53          115         120         125
54 Cys Gly Ser Ala Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala
55          130         135         140
56 Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu
57 145         150         155         160

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58 Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg
59                               165                               170                               175
60 Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr
61                               180                               185                               190
62 Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg
63                               195                               200                               205
64 Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys
65                               210                               215                               220
66 Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile
67 225                               230                               235                               240
68 Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile
69                               245                               250                               255
70 Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile
71                               260                               265                               270
72 Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn
73                               275                               280                               285
74 Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala
75                               290                               295                               300
76 Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
77 305                               310                               315                               320
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81 <211> LENGTH: 272
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Recombinant mutant Der p1 including pre-protein
88 <400> SEQUENCE: 2
89 Met Lys Ile Val Leu Ala Ile Ala Ser Leu Leu Ala Leu Ser Ala Val
90 1 5 10 15
91 Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala
92 20 25 30
93 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
94 35 40 45
95 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
96 50 55 60
97 Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
98 65 70 75 80
99 Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
100 85 90 95
101 Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln
102 100 105 110
103 Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys
104 115 120 125
105 Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr
106 130 135 140
107 Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala
108 145 150 155 160
109 Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr
110 165 170 175

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111 Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala
112          180          185          190
113 Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser
114          195          200          205
115 Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg Glu Ala
116          210          215          220
117 Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp
118 225          230          235          240
119 Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln Arg Asp
120          245          250          255
121 Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly Tyr Ser
122          260          265          270
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 320
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Recombinant mutant Der p1 including pre-protein -
132 His 258 to Ala 268
134 <400> SEQUENCE: 3
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136 1          5          10          15
137 Tyr Ala Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala
138          20          25          30
139 Phe Asn Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys
140          35          40          45
141 Asn Phe Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile
142          50          55          60
143 Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu
144 65          70          75          80
145 Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn
146          85          90          95
147 Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile
148          100          105          110
149 Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly
150          115          120          125
151 Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala
152          130          135          140
153 Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu
154 145          150          155          160
155 Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg
156          165          170          175
157 Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr
158          180          185          190
159 Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg
160          195          200          205
161 Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys
162          210          215          220
163 Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile

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164 225          230          235          240
165 Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile
166          245          250          255
167 Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr Ala Ala Val Asn Ile
168          260          265          270
169 Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn
170          275          280          285
171 Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala
172          290          295          300
173 Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
174 305          310          315          320
177 <210> SEQ ID NO: 4
178 <211> LENGTH: 339
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
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185 <400> SEQUENCE: 4
186 Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
187 1          5          10          15
188 Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
189          20          25          30
190 Ala His Ser Ala Phe Ala Ala Asp Pro Arg Pro Ser Ser Ile Lys Thr
191          35          40          45
192 Phe Glu Glu Tyr Lys Lys Ala Phe Asn Lys Ser Tyr Ala Thr Phe Glu
193          50          55          60
194 Asp Glu Glu Ala Ala Arg Lys Asn Phe Leu Glu Ser Val Lys Tyr Val
195 65          70          75          80
196 Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp
197          85          90          95
198 Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu
199          100          105          110
200 Lys Thr Gln Phe Asp Leu Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro
201          115          120          125
202 Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met
203          130          135          140
204 Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr
205 145          150          155          160
206 Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu
207          165          170          175
208 Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr
209          180          185          190
210 Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu
211          195          200          205
212 Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn
213          210          215          220
214 Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn
215 225          230          235          240
216 Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala

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217          245          250          255
218 Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly
219          260          265          270
220 Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala
221          275          280          285
222 Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile
223          290          295          300
224 Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr
225 305          310          315          320
226 Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val
227          325          330          335
228 Val Ile Leu
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233 <211> LENGTH: 343
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235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Recombinant mutant Der p1 encoded by pNIV4843
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243 Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
244          20          25          30
245 Ala His Ser Ala Phe Ala Ala Asp Pro Arg Pro Ser Ser Ile Lys Thr
246          35          40          45
247 Phe Glu Glu Tyr Lys Lys Ala Phe Asn Lys Ser Tyr Ala Thr Phe Glu
248          50          55          60
249 Asp Glu Glu Ala Ala Arg Lys Asn Phe Leu Glu Ser Val Lys Tyr Val
250 65          70          75          80
251 Gln Ser Asn Gly Gly Ala Ile Asn His Leu Ser Asp Leu Ser Leu Asp
252          85          90          95
253 Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu
254          100          105          110
255 Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn
256          115          120          125
257 Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr
258          130          135          140
259 Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Ala Trp Ala Phe Ser Gly
260 145          150          155          160
261 Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Gln Ser Leu
262          165          170          175
263 Asp Leu Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys
264          180          185          190
265 His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly
266          195          200          205
267 Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys
268          210          215          220
269 Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile
270 225          230          235          240

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VERIFICATION SUMMARY

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